

SEQUENCE LISTING

<110> Hellström, Mats
Wallgard, Elisabet
Kalén, Mattias

<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF

<130> 78063

<160> 52

<170> PatentIn version 3.2

<210> 1

<211> 736

<212> DNA

<213> Murinae gen. sp.

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<211> 306

<212> PRT

<213> Murinae gen. sp.

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Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly
35 40 45

Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu
50 55 60

Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser
65 70 75 80

Val Thr Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala
85 90 95

His Gly Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys
100 105 110

Gly Ala Trp Pro Ser Ile Leu Leu Ser Val Gln Asn Val Ile Asp Cys
115 120 125

Gly Asn Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Pro Val Trp Glu
130 135 140

Tyr Ala His Lys His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln
145 150 155 160

Ala Lys Asp Gln Asp Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Thr
165 170 175

Glu Phe Lys Glu Cys His Thr Ile Gln Asn Tyr Thr Leu Trp Arg Val
180 185 190

Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile
195 200 205

Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met
210 215 220

Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val
225 230 235 240

Ile Asn His Ile Ile Ser Val Ala Gly Trp Gly Val Ser Asn Asp Gly
245 250 255

Ile Glu Tyr Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu
260 265 270

Lys Gly Trp Met Arg Ile Val Thr Ser Thr Tyr Lys Gly Gly Thr Gly
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Asp Ser Tyr Asn Leu Ala Ile Glu Ser Ala Cys Thr Phe Gly Asp Pro
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<211> 1480

<212> DNA

<213> Homo sapiens

<400> 4

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<210> 5
<211> 303
<212> PRT
<213> Homo sapiens

<400> 5

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Cys Tyr Arg Pro Leu Arg Gly Asp Gly Leu Ala Pro Leu Gly Arg Ser
35 40 45

Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
50 55 60

Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr
65 70 75 80

Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala
85 90 95

Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala
100 105 110

Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn
115 120 125

Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala
130 135 140

His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys
145 150 155 160

Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe
165 170 175

Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp
180 185 190

Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala
195 200 205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn
210 215 220

Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn
225 230 235 240

His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr
245 250 255

Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp
260 265 270

Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr
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Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val
290 295 300

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<211> 646
<212> DNA
<213> Murinae gen. sp.

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240

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420

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<212> DNA
<213> Murinae gen. sp.

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<211> 536
<212> PRT
<213> Murinae gen. sp.

<400> 8

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Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu
35 40 45

Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser
50 55 60

Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr
65 70 75 80

Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg
85 90 95

Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu
100 105 110

Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr
115 120 125

Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val
130 135 140

Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln
145 150 155 160

Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser
165 170 175

Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe
180 185 190

Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn
195 200 205

Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro
210 215 220

Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser
225 230 235 240

Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr
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Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly
260 265 270

His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys
275 280 285

Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr
290 295 300

Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser
305 310 315 320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu
325 330 335

Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg
340 345 350

Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys
355 360 365

Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp
370 375 380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val
385 390 395 400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr
405 410 415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu
420 425 430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu
435 440 445

Asn Phe Glu Gly Ser Glu Lys Gln Lys Gln Leu Val Ile Gly Gly Glu
450 455 460

Ala Cys Leu Trp Gly Glu Phe Val Asp Ala Thr Asn Leu Thr Pro Arg
465 470 475 480

Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg Leu Trp Ser Pro Lys
485 490 495

Thr Val Thr Asp Leu Glu Asn Ala Tyr Lys Arg Leu Ala Val His Arg
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Cys Arg Met Val Ser Arg Gly Ile Ala Ala Gln Pro Leu Tyr Thr Gly
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Tyr Cys Asn Tyr Glu Asn Lys Ile
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<210> 9
<211> 1746
<212> DNA
<213> Homo sapiens

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<210> 10
<211> 556
<212> PRT
<213> Homo sapiens

<400> 10

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Val Ala Leu Val Val Gln Val Ala Glu Ala Ala Arg Ala Pro Ser Val
35 40 . 45

Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Leu Val Lys
50 55 60

Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
65 70 75 80

His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
85 90 95

Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
100 105 110

His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
115 120 125

Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
130 135 140

Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
145 150 155 160

Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
165 170 175

Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
180 185 190

Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
195 200 205

Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
210 215 220

Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
225 230 235 240

Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
245 250 255

Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
260 265 270

Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu

275

280

285

Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp
290 295 300

Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly
305 310 315 320

Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe
325 330 335

Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly
340 345 350

Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln
355 360 365

Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu
370 375 380

Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys
385 390 395 400

Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala
405 410 415

Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu
420 425 430

Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro
435 440 445

Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr
450 455 460

Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Gln Leu
465 470 475 480

Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr
485 490 495

Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg
500 505 510

Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg
515 520 525

Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
530 535 540

Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met
545 550 555

<210> 11
<211> 676
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<222> (604)..(604)
<223> n is a, c, g, or t

<400> 11
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ctccatcatc gggcgccctgc tggaagtgca gggctcacgg cctgggaaga acgtgcagct
120

gacagagaac gagatccgtg gtctgtgcct caaatcccgagatttcc tgagccagcc
180

cattcttctg gagcttgagg cgcgcctcaa gatctgtggt gacatccatg gccagacta
240

tgaccttcta cggctgtttg agtatggtg cttccctcca gagagcaact acctcttctt
300

gggggattat gtagatcgaa gcaagcagtc tttggagacc atctgcctgt tgctggccta
360

taagatcaga taccggaga atttcttct acttcgtgg aaccatgagt gtgccagcat
420

caaccgcatt tatggcttct atgatgaatg caagagaaga tacaacatca aactgtggaa
480

gacgttcact gactgcttca actgcctgcc cattgcagcc attgtggatg agaagatctt
540

ctgctgccac gggggcctgt ctccagactt gcaatccatg gagcagatggat ggcgtattat
600

gcgngccaca gacgtgcctg accagggcct actgtgtat ctccctgtggt ctgaccctga
660

caagaaatag cctcca
676

<210> 12
<211> 1369

<212> DNA

<213> Murinae gen. sp.

<400> 12

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cgagaagctc aacctggact ccatcatcg ggccctgctg gaagtgcagg gtcacggcc
120

tgggaagaac gtgcagctga cagagaacga gatccgttgt ctgtgcctca aatccggga
180

gattttcctg agccagccca ttcttctgga gcttgaggcg cccctcaaga tctgtggta
240

catccatggc cagtactatg accttctacg gctgttttag tatggtggt tccctccaga
300

gagcaactac ctcttcttgg gggattatgt agatcggggc aagcagtctt tggagaccat
360

ctgcctgttg ctggcctata agatcagata cccggagaat ttctttctac ttcgtggaa
420

ccatgagtgt gccagcatca accgcattta tggcttctat gatgaatgca agagaagata
480

caacatcaaa ctgtggaaga ctttcactga ctgcttcaac tgcctgcaca ttgcagccat
540

tgtggatgag aagatcttct gctgccacgg gggcctgtct ccagacttgc aatccatgga
600

gcagattagg cgtattatgc gcccacaga cgtgcctgac cagggcctac tgtgtgatct
660

cctgtggtct gaccctgaca agatgttca aggctggggc gagaatgacc gtgggtctc
720

ctttacctt gggctgagg tggtagccaa gttcctgcac aagcatgatt tggacctcat
780

ctgcagagca catcagggtt tagaagatgg ctatgagttc tttgccaaga gacagtttgt
840

gacactcttc tcagctccca actactgtgg agagtttgc aatgctggtg ccatgatgag
900

tgtggatgag accctcatgt gttccttcca gatcctcaag cccgctgata agaataaggg
960

caagtatggg cagttcagcg gcctgaaccc cggaggccgg cccatcactc caccccgcaa
1020

ttctgccaaa gccaagaaat agcctccatg tgctgccctt ctgccccaga tcgtttgtac
1080

agaaatcatg ctgccatggg tcacactggc ctctcaggcc caccctgtcac gggaaacaca
1140

cagcgtaag tgtcttcct ttattttta aagaatcaat agcagcatct aatctccag
1200

ggctccctcc caccagcacc tgtggtggct gcaagtggaa tcctggggcc aaggctgcag
1260

ctcaggcaaa tggcagacca gattgtgggt ctccagcatt gcatggctgg cagccagatc
1320

ctggggcaac ccatctggtc tcttgaataa aggtcaaagc tggattctc
1369

<210> 13

<211> 330

<212> PRT

<213> Murinae gen. sp.

<400> 13

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
100 105 110

Arg Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu

165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305 310 315 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
325 330

<210> 14

<211> 993

<212> DNA

<213> Homo sapiens

<400> 14

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120

aaatcccgaa agattttct gagccagccc attcttctgg agctggaggc acccctcaag
180

atctgcggtg acatacacgg ccagtactac gaccttctgc gactattga gtatggcggt
240

ttccctcccc agagcaacta cctctttctg gggactatg tggacagggg caagcagtcc
300

ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg
360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc
420

aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc
480

atcgcgcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg
540

cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg
600

ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac
660

cgtggcgtct ctttacctt tggagccgag gtggtggcca agttcctcca caagcacgac
720

ttggacctca tctgcccggc acaccaggtg gtagaagacg gctacgagtt cttgccaag
780

cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagttga caatgctggc
840

gccatgatga gtgtggacga gaccctcatg tgctcttcc agatcctcaa gcccggcgc
900

aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc
960

ccaccccgca attccgccaa agccaagaaa tag
993

<210> 15
<211> 330
<212> PRT
<213> Homo sapiens

<400> 15

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Ala Tyr Lys Ile
100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305 310 315 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
325 330

<210> 16
<211> 702
<212> DNA
<213> Murinae gen. sp.

<400> 16
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ggctgctgga gatatggctg tggctcacaa ggaggctggg gaactagcaa ggagatgctc
120

tctcagctat cacagcctta cagcaaagcc actatctttt tggattttga aattttctct
180

gccatgccta tgactatttt aaaattgggc aaagtatac catttcagag gggcttttc
240

tgtactgaca acagcgtgaa gtacccgtac catgacagta ccatccgtc ccgtataactc
300

gccatactgg ggcttggctt acccattttc tctatgagta tggagaatct ctgtctgttt
360

actttaatgt cttgcattcg aattcctttt tcggcaatcc ctacatagcc accattaca
420

aagccgtcgg agcctttgt tcggagtctc agctagtcg tccttgactg acatcgctaa
480

gtatactata ggcagtttgc ggccgcactt cttggctatc tgtaaccagg actggtaaa
540

aatcaactgc agtgatggct atattgagga ctacatatgt caaggaaatg aagagaaatg
600

caaggagggc aggttgtctt tctactcggtt acactcttca ttctctatgt actgcgtgt
660

gtttgtcgca ctttatcttc aagccaggat gaaggagac tg
702

<210> 17
<211> 1432
<212> DNA
<213> Murinae gen. sp.

<400> 17
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gcgacgagcc agcactgaga gagcaggcgc ctgaggcgac agatcgccgg ccactcggtg
120
gcagggcggc ccaatccaaa ctgccttgtt ccctgctccc gtcagtctaa gaggctcgca
180
gtcgcttggg gcggccgcca tcccggggc gggctctgg gaattggta tctggaccgc
240
cgcggtctgt tcctcccgcc actcgacca ggtggtgaca ccatccagcc ggtgaccatg
300
ttcgacaaga cgcggtgtcc gtacgtggcc ctcgatgtga tttgcgtgtt gctggctgga
360
ttgccttttgc caatttttac ttcaaggcat acccccttcc agcgaggaat attctgttaat
420
gatgactcca tcaagtaccc ttacaaggaa gacaccatac cttatgcctt attaggtgga
480
atagtcatttc cattctgtat tatcgttatg agtattggag aatctctgtc tgtttacttt
540
aatgtcttgc attcgaattt ctttgcggc aatccctaca tagccaccat ttacaaagcc
600
gtcggagcct ttttgcggc agtctcagct agtcagtcct tgactgacat cgctaagtat
660
actataggca gtttgcggcc gcacttcttg gctatctgtt acccagactg gtcaaaaatc
720
aactgcagtg atggctatat tgaggactac atatgtcaag ggaatgaaga gaaagtcaag
780
gagggcaggt tgtctttcta ctcggacac tcttcattct ctatgtactg catgctgttt
840
gtcgcacttt atcttcaagc caggtgaag ggagactggg caagacttt acgaccatg
900
ctccagtttgc ggctcattgc ttttccata tatgtggcc tttctcgagt gtctgactac
960
aaacaccact ggagtgacgt cacagttgga ctcattcagg gagctgctat ggctatactg
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gttgctttgt atgtatccga tttcttcaag gacacacatt cttacaaaga gagaaaggaa
1080
gaggatccac acacgactct ccatgaaacc gccagttcac ggaactactg ggcgctggcc
1140
cgcttcaaag gcaacagctg gaggttaaag gcagggggat gcgttattact tcctgctgtt
1200
cagaccatttca tataaaggac tgctgctatc tatacctcct ggatgccat tttatgtgtt
1260

tacagttact tctaacacaa tgagtaacag ttcaattaaa gaaaatgaag cctgtcacta
1320

aaacactgtc ccacacctgtac atttttattt aaagacgcta tgtacaaatg tgtatgttac
1380

atgccttctc agaatgatgt tgacttaaat ataataaaaa gcttgtgaac ca
1432

<210> 18
<211> 378
<212> PRT
<213> Murinae gen. sp.

<400> 18

Glu Ser Arg Arg Leu Arg Arg Gln Ile Gly Gly His Ser Val Ala Gly
1 5 10 15

Arg Pro Asn Pro Asn Cys Pro Gly Pro Cys Ser Arg Gln Ser Lys Arg
20 25 30

Leu Ala Val Ala Trp Gly Gly Arg His Pro Glu Gly Gly Ala Leu Gly
35 40 45

Ile Gly Tyr Leu Asp Arg Arg Gly Leu Phe Leu Pro Pro Leu Ala Pro
50 55 60

Gly Gly Asp Thr Ile Gln Pro Val Thr Met Phe Asp Lys Thr Arg Leu
65 70 75 80

Pro Tyr Val Ala Leu Asp Val Ile Cys Val Leu Leu Ala Gly Leu Pro
85 90 95

Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg Gly Ile Phe
100 105 110

Cys Asn Asp Asp Ser Ile Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro
115 120 125

Tyr Ala Leu Leu Gly Gly Ile Val Ile Pro Phe Cys Ile Ile Val Met
130 135 140

Ser Ile Gly Glu Ser Leu Ser Val Tyr Phe Asn Val Leu His Ser Asn
145 150 155 160

Ser Phe Val Gly Asn Pro Tyr Ile Ala Thr Ile Tyr Lys Ala Val Gly
165 170 175

Ala Phe Leu Phe Gly Val Ser Ala Ser Gln Ser Leu Thr Asp Ile Ala
180 185 190

Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu Ala Ile Cys Asn
195 200 205

Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Asp Tyr
210 215 220

Ile Cys Gln Gly Asn Glu Glu Lys Val Lys Glu Gly Arg Leu Ser Phe
225 230 235 240

Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala
245 250 255

Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg
260 265 270

Pro Met Leu Gln Phe Gly Leu Ile Ala Phe Ser Ile Tyr Val Gly Leu
275 280 285

Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Thr Val Gly
290 295 300

Leu Ile Gln Gly Ala Ala Met Ala Ile Leu Val Ala Leu Tyr Val Ser
305 310 315 320

Asp Phe Phe Lys Asp Thr His Ser Tyr Lys Glu Arg Lys Glu Glu Asp
325 330 335

Pro His Thr Thr Leu His Glu Thr Ala Ser Ser Arg Asn Tyr Trp Ala
340 345 350

Leu Ala Arg Phe Lys Gly Asn Ser Trp Arg Leu Lys Ala Gly Gly Cys
355 360 365

Val Leu Leu Pro Ala Val Gln Thr Ile Leu
370 375

<210> 19
<211> 1626
<212> DNA
<213> Homo sapiens

<400> 19
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gagtctggac gccccgcctg tggagagag cggcgggatc cggacgggga gcaaccgggg
120
caggccgtgc cggctgagga ggtcctgagg ctacagagct gccgcggctg gcacacgagc
180
gcctcggcac taaccgagtg ttgcgggggg ctgtgagggg agggcccccgg gcccattgc
240
tggcggtggg agcgccgccc ggtctcagcc cgcctcggc tgctctcctc ctccggctgg
300
gaggggccgt agctcggggc cgtcgccagc cccggcccccgg gtcgagaat caagggcctc
360
ggccgcccgtc ccgcagctca gtccatcgcc cttgccgggc agcccgggca gagaccatgt
420
ttgacaagac gcggctgccc tacgtggccc tcgatgtgct ctgcgtgttg ctggcttcca
480
tgcctatggc tggcttaaaa ttggccaaa tatattcatt tcagagaggc ttttctgta
540
aagacaacag catcaactat ccgtaccatg acagtaccgt cacatccact gtcctcatcc
600
tagtgggggt tggcttgcctt atttcctcta ttattcttgg agaaaccctg tctgtttact
660
gtaacccccc gcactcaaattt tcctttatca ggaataacta catagccact atttacaaag
720
ccattggaac ctttttattt ggtcagctg ctagtcagtc cctgactgac attgccaagt
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ttgtggcact ttatcttcaa gccaggatga agggagactg ggcaagactc ttacgccccca
1020
cactgcaatt tggtcttggt gccgtatcca tttatgtggg ctttctcga gtttctgatt
1080
ataaacacca ctggagcgat gtgttgactg gactcattca gggagctctg gttgcaatat
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1200
aggaggactc tcataacaact ctgcattgaaa caccaacaac tggaaatcac tatccgagca
1260

atcaccagcc ttgaaaggca gcagggtgcc caggtgaagc tggcctgttt tctaaaggaa
1320

aatgattgcc acaaggcaag aggatgcac tttcttcctg gtgtacaagc ctttaagac
1380

ttctgctgct gctatgcctc ttggatgcac actttgtgtg tacatagttt cctttaactc
1440

agtggttatc taatagctct aaactcatta aaaaaactcc aagccttcca ccaaaacagt
1500

gccccacctg tatacatttt tattaaaaaa atgtaatgct tatgtataaa catgtatgt
1560

atatgcttc tatgaatgat gtttgattt aatataatac atattaaaat gtatggaga
1620

accaaa
1626

<210> 20
<211> 378
<212> PRT
<213> Homo sapiens

<400> 20

Gly Gly Pro Glu Ala Thr Glu Leu Pro Arg Leu Ala His Glu Arg Leu
1 5 10 15

Gly Thr Asn Arg Val Phe Ala Gly Ala Val Arg Gly Gly Pro Arg Ala
20 25 30

Pro Leu Leu Ala Val Gly Ala Pro Pro Gly Leu Ser Pro Pro Ser Ala
35 40 45

Ala Leu Leu Leu Arg Leu Gly Gly Ala Val Ala Arg Gly Arg Arg Gln
50 55 60

Pro Arg Pro Gly Leu Glu Asn Gln Gly Pro Arg Pro Pro Ser Arg Ser
65 70 75 80

Ser Val His Arg Pro Cys Arg Ala Ala Arg Ala Glu Thr Met Phe Asp
85 90 95

Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu
100 105 110

Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe
115 120 125

Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His
130 135 140

Asp Ser Thr Val Thr Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu
145 150 155 160

Pro Ile Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn
165 170 175

Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile
180 185 190

Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser
195 200 205

Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe
210 215 220

Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly
225 230 235 240

Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu
245 250 255

Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys
260 265 270

Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp
275 280 285

Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser
290 295 300

Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser
305 310 315 320

Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val
325 330 335

Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu
340 345 350

Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr
355 360 365

Gly Asn His Tyr Pro Ser Asn His Gln Pro

370

375

<210> 21
<211> 816
<212> DNA
<213> Homo sapiens

<400> 21
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ttccaacgag gagtattctg taatgatgag tccatcaagt acccttacaa agaagacacc
120

atacctttagt cgtttattagg tggaataatc attccattca gtattatcg tattattctt
180

ggagaaaaccc tgtctgttta ctgtaacctt ttgcactcaa attcctttat caggaataac
240

tacatagcca ctatttacaa agccattgga accttttat ttgggtgcagc tgctagtcag
300

tccctgactg acattgccaa gtattcaata ggcagactgc ggcctcactt cttggatgtt
360

tgtgatccag attggtcaaa aatcaactgc agcgatggtt acattgaata ctacatatgt
420

cgagggaaatg cagaaagagt taaggaaggc aggttgcct tctattcagg ccactctcg
480

ttttccatgt actgcatgct gtttggca ctttatcttc aagccaggat gaagggagac
540

tgggcaagac tcttacgccc cacactgcaa tttggcttg ttgccgtatc catttatgtg
600

ggcctttctc gagttctga ttataaacac cactggagcg atgtgttgc tggactcatt
660

cagggagctc tggttgcaat attagttgct gtatatgtat cggatttctt caaagaaaga
720

acttctttta aagaaagaaa agaggaggac tctcatacaa ctctgcataa aacaccaaca
780

actggaaatc actatccgag caatcaccag ccttga
816

<210> 22
<211> 271
<212> PRT
<213> Homo sapiens

<400> 22

Ile Tyr Ser Leu Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser
1 5 10 15

Arg His Thr Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile
20 25 30

Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly
35 40 45

Ile Ile Ile Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu
50 55 60

Ser Val Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn
65 70 75 80

Tyr Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala
85 90 95

Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg
100 105 110

Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile
115 120 125

Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala
130 135 140

Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser
145 150 155 160

Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg
165 170 175

Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly
180 185 190

Leu Val Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr
195 200 205

Lys His His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu
210 215 220

Val Ala Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg
225 230 235 240

Thr Ser Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His
245 250 255

Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
260 265 270

<210> 23
<211> 840
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<222> (474)..(474)
<223> n is a, c, g, or t

<400> 23
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ctgactgaga agaggacgct cccgggaaac gaatgaggaa ccacccctc ctgctgttca
120

agtacagggg cctggtgcgaa aaaggaaaga aaagcaaaag acgaaaatgg ctaaatttaa
180

gatccgtcca gccactgcct ctgactgcag tgacatcctg cgactgatca aggaactggc
240

taaatatgaa tacatggaag atcaagtcat tttaactgag aaagatctcc aagaggatgg
300

cttggagaa cacccttctt accactgcct gggtgcagaa gtgcctaaag agcactggac
360

ccctgaagga catagcattt ttgggttcgc catgtactat tttacctatg acccatggat
420

tggcaagttt ctgtatctt aagacttctt cgtgatgagt gattacagag gctntggat
480

aggatcagaa attttgaaga atctaagcca gggtgcctt aagtgtcgct gcagcagtat
540

gcacttcttgc gtagcagaat ggaatgaacc atctatcaac ttctacaaaaa gaagaggtgc
600

ttcggatctt tccagtgaag agggatggga ggctcttcaa gattgacaag agtacttgct
660

aaaaatggca gcagaggagt gaggcgtgcc ggtgtagaac atgacaacct ccattgtgct
720

ttagaataat tctcagcttc ctttgcttca tatcttggat tgttaggtgaa ataataagagc
780

gagccaccat tccaaagctt tattaccagt qacgtqttqc atqttqaaa tcgggtctqgt

6210 > 34

<211> 1052
<212> DNA
<213> Murinae gen. sp.

<400> 24
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gtcatggtgc cagcctgact gagaagagga cgctcccgaa aacgaatga ggaaccaccc
120
cctcctgctg ttcaagtaca ggggcctggt gcgcaaagg aagaaaagca aaagacgaaa
180
atggctaaat ttaagatccg tccagccact gcctctgact gcagtgacat cctgcgactg
240
atcaaggaac tggctaaata tgaatacatg gaagatcaag tcattttaac tgagaaagat
300
ctccaagagg atggctttgg agaacacccc ttctaccact gcctgggtgc agaagtgcct
360
aaagagcact ggaccctga aggacatagc attgttgggt tcgccatgta ctatttacc
420
tatgaccat ggattggcaa gttgctgtat cttgaagact tcttcgtat gagtgattac
480
agaggcttg gtataggatc agaaattttg aagaatctaa gccaggttgc catgaagtgt
540
cgctgcagca gtatgcactt cttggtagca gaatggaatg aaccatctat caacttctac
600
aaaagaagag gtgcttcgga tctgtccagt gaagagggat ggaggcttt caagattgac
660
aaagagtact tgctaaaaat ggcagcagag gagtgaggcg tgccgggtgt gacaatgaca
720
acctccattt tgcttttagaa taattctcag cttcccttgc tttctatctt gtgtgttagtg
780
aaataataga gcgagcaccc attccaaagc tttattacca gtgacgttgt tgcatgtttg
840
aaattcggtc tgtttaaagt ggcagtcatg tatgtggttt ggaggcagaa ttcttgaaca
900
tcttttgcatg aagaacaagg tggatgtac ttactatata agaaaaacaa aacttcattc
960
ttgtgagtca tttaaatgtg tacaatgtac acactggtagtac ttagagtttc tgttttgatt
1020
cttttttttt taaataaact actctttgat tt
1052

<210> 25

<211> 171
 <212> PRT
 <213> Murinae gen. sp.

<400> 25

Met Ala Lys Phe Lys Ile Arg Pro Ala Thr Ala Ser Asp Cys Ser Asp
 1 5 10 15

Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met Glu Asp
 20 25 30

Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu
 35 40 45

His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp
 50 55 60

Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr
 65 70 75 80

Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val
 85 90 95

Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn
 100 105 110

Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu
 115 120 125

Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly
 130 135 140

Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp
 145 150 155 160

Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu
 165 170

<210> 26
 <211> 1111
 <212> DNA
 <213> Homo sapiens

<400> 26

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tcatggtgcc agcctgactg agaagaggac gctccggga gacgaatgag gaaccaccc
 120

ctcctactgt tcaagtacag gggcctggtc cgcaaaggga agaaaagcaa aagacgaaaa
180

tggctaaatt cgtgatccgc ccagccactg ccgccgactg cagtgacata ctgcggctga
240

tcaaggagct ggctaaatat gaatacatgg aagaacaagt aatcttaact gaaaaagatc
300

tgctagaaga tggtttgga gagcacccct tttaccactg cctggttgca gaagtgccga
360

aagagcactg gactccggaa ggtaacccct cgccctttcc agaagccaga gagaccaaca
420

ttgttggttt tgccatgtac tattttacct atgaccgcgt gattggcaag ttattgtatc
480

ttgaggactt ctgcgtgatg agtgattata gaggtacgt tgagcttgg cataggatca
540

gaaattctga agaatctaag ccaggttgca atgaggtgtc gctggcagca tgcacttctt
600

gggcagaatg gaatgaacca tccatcaact tctataaaag aagaggtgct tctgatctgt
660

ccagtgaaga gggttggaga ctgttcaaga tcgacaagga gtacttgcta aaaatggcaa
720

cagaggagtg aggagtgcgt ctgtagatga caacccat tctatttag aataaattcc
780

caacttctct tgctttctat gctgttgta gtgaaataat agaatgagca cccattccaa
840

agctttatta ccagtggcgt tggcatgt ttgaaatgag gtctgtttaa agtggcaatc
900

tcagatgcag tttggagagt cagatcttc tccttgaata tcttcgata aacaacaagg
960

tggtgtgatc ttaatatatt tgaaaaaaac ttcattctcg tgagtcattt aaatgtgtac
1020

aatgtacaca ctggactta gagttctgt ttgattctt ttataataac tactcttga
1080

tttaattcta aaaaaaaaaa aaaaaaagac a
1111

<210> 27
<211> 190
<212> PRT
<213> Homo sapiens

<400> 27

Glu Pro Pro Pro Pro Thr Val Gln Val Gln Gly Pro Gly Pro Gln Arg

1

5

10

15

Glu Glu Lys Gln Lys Thr Lys Met Ala Lys Phe Val Ile Arg Pro Ala
20 25 30

Thr Ala Ala Asp Cys Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu Ala
35 40 45

Lys Tyr Glu Tyr Met Glu Glu Gln Val Ile Leu Thr Glu Lys Asp Leu
50 55 60

Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Val Ala
65 70 75 80

Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly Asn Pro Ser Pro Phe
85 90 95

Pro Glu Ala Arg Glu Thr Asn Ile Val Gly Phe Ala Met Tyr Tyr Phe
100 105 110

Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe
115 120 125

Val Met Ser Asp Tyr Arg Gly Thr Ile Glu Leu Trp His Arg Ile Arg
130 135 140

Asn Ser Glu Glu Ser Lys Pro Gly Cys Asn Glu Val Ser Leu Ala Ala
145 150 155 160

Cys Thr Ser Trp Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys
165 170 175

Arg Arg Gly Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg
180 185 190

<210> 28

<211> 745

<212> DNA

<213> Murinae gen. sp.

<400> 28

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tttgtatct ttgggtgtct gaccccgatg aaagatgtct taggctgggg tgaaaatgac
120

agaggagtgt cttcacatt tggtgagaa gtggttgcaa aatttctcca taagcatgat
180

tcggatctta tatgttaggc ccatcagggtg gttgaagatg gctatgagtt tttcgcaaag
240
aggcagttag tcactctgtt gttctgcgag cccaaactact gtggcgagtt tgacaatgca
300
ggcgccatga tgagtgtgga tgagaccctc atgtgttcct tccagattt aaagcctgca
360
gagaaaaaga agcccaacgc cacgagacct gtcacaccac cacgggtat gatcacaaag
420
caagcaaaga aatagatgtc acttgacact gcctgggtgg gacttgtaac atagcggtca
480
taaccttcct ttttaaactg tcatgtgtgc gtcagcttgc ccaggtagac ctgtctgtcg
540
ggccctcctc catttgatta ctgctggcac ttgctggta tagcagcaag ccaagcactt
600
cattctcaag agagcatttg gttctgaacc tctgttcct ttgtggacag ctctgtatgt
660
ggtgttaagc tgtacaccct ggcaggttat cctgtctgag gagaaagtgt acaattgtac
720
tttttttagt ttagtataag tcatg
745

<210> 29
<211> 2127
<212> DNA
<213> Murinae gen. sp.

<400> 29
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acagcatcat ccaacggctg ctggaagtga gagggtccaa gccaggcaag aatgtccagc
120
tccaggagaa cgagatccga ggactctgcc tgaagtctcg ggagatcttc ctcagtcagc
180
ctatcccttt agaacttgaa gcaccactca agatatgtgg tgacatccac gggcagtact
240
atgatttgct ccgtctgttt gaatacggtg gctttcctcc agagagcaac tatttggttc
300
tcggggacta tgtggacagg ggcaaggcagt ccctggagac aatctgcctc ttgctggcct
360
acaaaatcaa gtatccggag aacttcttcc ttctcagagg gaaccacgag tgcgccagca
420
tcaataggat ctacggattt tatgtatgagt gtaaaagaag atacaacatt aagctgtgga
480

aaacgttcac agactgtttt aactgcttgc cgatagcagc catcggtggac gagaagat 540
540
tctgctgtca tggaggttta tcaccagatc ttcaatctat ggagcagattt cggcgaatta 600
600
tgagaccaac ttagtacca gatcaaggc ttctttgtga tctttgtgg tctgaccgg 660
660
ataaagatgt cttaggctgg ggtgaaaatg acagaggagt gtccttcaca tttgggtgcag 720
720
aagtggttgc aaaatttctc cataagcatg atttggatct tatatgtaga gcccattcagg 780
780
tggttgaaga tggctatgag tttttgcaa agaggcattt agtcactctg ttttctgcac 840
840
ccaactactg tggcgagttt gacaatgcag gcgcattatgat gagtggat gagaccctca 900
900
tgtgttcctt ccagatttta aagcctgcag agaaaaagaa gcccaacgcc acgagacctg 960
960
tcacaccacc acggggatag atcacaaagc aagcaaagaa atagatgtca cttgacactg 1020
1020
cctgggtggg acttgtaaca tagcgatcat aaccttcctt tttaactgt gatgtgctgg 1080
1080
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1140
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1500
tggcagcagg agtgcacccgc ctggcccgccag ccctgcccag actatctgaa gcacactcct 1560
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1620
aaagccaaag tttctgttgg actgtatggc acgcctggg gatgagggtgg ccagggcatc 1680
1680

gaggctgcgt gcacaggccg cctccctccg tggggcctca gaagcaggtt attttaacta
1740

gcaatagtgg tatagtgctg agtaagctat taatgatgga agttaatgac actttgtaca
1800

gttcccatat agtctattca ctgagtgatc ttttacagt tggatcaggc ctgaaccggt
1860

ccattcagaa agcttcaaat tatagaaaca acactgtcct atacgagtga ccgataatgc
1920

tttctttggc tacattctt attctgcggt gacattgagg ctataaaatc aaaaggaaact
1980

aacttgccgt ccaccggttt atacagaact cacagtatct atgactttt taaactacga
2040

cctgttaaat gaatctgttt gcacagatgc ccgtgtacaa tgccatgtgc tgagaatgg
2100

ttcagactta ttaaatgcaa gcttgaa
2127

<210> 30

<211> 323

<212> PRT

<213> Murinae gen. sp.

<400> 30

Met Ala Asp Ile Asp Lys Leu Asn Ile Asp Ser Ile Ile Gln Arg Leu
1 5 10 15

Leu Glu Val Arg Gly Ser Lys Pro Gly Lys Asn Val Gln Leu Gln Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala

115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
195 200 205

Pro Asp Lys Asp Val Leu Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Glu Lys Lys Lys Pro
290 295 300

Asn Ala Thr Arg Pro Val Thr Pro Pro Arg Gly Met Ile Thr Lys Gln
305 310 315 320

Ala Lys Lys

<210> 31
<211> 993
<212> DNA
<213> Homo sapiens

<400> 31

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120
aaatcccgaa agattttct gagccagccc attttctgg agctggaggg acccctcaag
180
atctgcggtg acatacacgg ccagtactac gacccctgc gactattta gtatggcggt
240
ttccctcccg agagcaacta cctctttctg gggactatg tggacagggg caagcagtcc
300
ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg
360
ctccgtggaa accacgagtg tgccagcatc aaccgcatct atggttctta cgatgagtgc
420
aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc
480
atcgccggcca tagtgacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg
540
cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg
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660
cgtggcgtct ctttacctt tggagccgag gtggcggcca agttcctcca caagcacgac
720
ttggacactca tctgcccggc acaccaggta gtagaagacg gctacgagtt ctttgccaaag
780
cgccagctgg tgacacttt ctcagctccc aactactgtg gcgagttga caatgctggc
840
gccatgatga gtgtggacga gaccctcatg tgctcttcc agatcctcaa gcccgcgcac
900
aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc
960
ccaccccgca attccgccaa agccaaagaaa tag
993

<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

<400> 32

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Ala Tyr Lys Ile
100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305 310 315 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
325 330

<210> 33
<211> 747
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<222> (298)..(298)
<223> n is a, c, g, or t

<400> 33
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ttcggtggcc tgtatgacct ggacgcctct cgctacttcg tccttctgcc tctgtgcctc
120

tgcgtatgg ttgagctggg agagtagccc agtggtagac agccccaccc gaataacttg
180

ggacctgggg ttgtctccca gcactgcaaa agaaaaattc actgttacag tcttccttgc
240

acttaaacca gctttgtcta ttgtttttt ggtttggctt tgttactttt gttgctgntt
300

atttttgtt gttttttt gttttttt gttttttt gttttttt gttttttt gttttttt
360

tgaaactccc tctgttagacc aggctggcct caaacttaca gagatccgcc tgcctcagcc
420

tcccaagtgc tggaaataat ggtgtggtca ccaccgccc gcctttgtc tattttaaa
480

cttggaaagaa acaacagccc agatttcaaa aataatataa tgcacttata ctaaaaaaaa
540

caaccaggag tgcccagtta ataacatttt ttaaatgtgg ggatgggaag ggcatttagag
600

gagtcttcct tctattgaag attcattaaa gtatttaaga tatgccctt cactctttat
660

ataaatccaa gattttctt tgctgaagta tttaaaactt ttgtacctt atatgttagat
720

atgaatttga aaatatgctt atgtgtat
747

<210> 34

<211> 2021

<212> DNA

<213> Murinae gen. sp.

<400> 34

ggccaagaaa cttcaacaga agtccacacc tccccagaag catccgtcaa agagggacga
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gcagaccgag caaacactcc cagcgccaaa gatcgggact gtgggaaatc tgcagggccc
120

agttccaagc tctctggaa ccggaacggc agggaaagcc gagcgggccc cctgaaggag
180

agaagcaatg gatcagaggg ggctccaagt 'gaaggaaggg taagtccaaa gagcagcgat
240

cctgagactg gcctgataga ctgcagcact tcacaggccg ccagttctcc agaaccacc
300

agcctaagg gctccacatc tctgcctgtt cactcagctt ccagagctag gaaagagcag
360

ggtgctggca gccattccga cgcttgaaga aaactgtctc gttccccag aagcacatgt
420

atgttacact ggagatgacc aactgatttg tcttataaag gccactgttg agctggaga
480

gtagccagt ggtacagcgc ccacctggaa tacttgagga cctggggttg tctccagca
540

ctgcaaaagg aaaattcact gttacagtct tcctgcact taaaccagct ttgtctattg
600

tttttttgtt ttggctttta ttttgttg ttttattttt gttgttgtt gtttgtttt
660

ttgtttgttt gttttagaca gggtttcttt gctagccctg actgtcctga aactccctct
720

gtagaccagg ctggcctcaa acttacagag atctgcctgc ctcagcctcc cgagtgtgg
780

gaataatggt gtggtcacca ctgcccagcc ttttgtctgt ttttaaactt gaaagaaaaca
840

<210> 35
<211> 709
<212> PRT
<213> Murinae gen. sp.

<400> 35

Met Glu Arg Ser Pro Phe Leu Leu Ala Cys Ile Leu Leu Pro Leu Val
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Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Thr Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Gly Ile Ala Ala Val Glu Met Gly His Phe Leu His Leu
50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Met Phe Leu Cys Gln Ala
65 70 75 80

Phe Ile Pro Thr Cys Thr Glu Gln Ile His Val Val Leu Pro Cys Arg
85 90 95

Lys Leu Cys Glu Lys Ile Val Ser Asp Cys Lys Lys Leu Met Asp Thr
100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asn Arg Leu Pro His
115 120 125

Cys Asp Asp Thr Val Pro Val Thr Ser His Pro His Thr Glu Leu Ser
130 135 140

Gly Pro Gln Lys Lys Ser Asp Gln Val Pro Arg Asp Ile Gly Phe Trp
145 150 155 160

Cys Pro Lys His Leu Arg Thr Ser Gly Asp Gln Gly Tyr Arg Phe Leu
165 170 175

Gly Ile Glu Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
180 185 190

Asp Glu Leu Asp Phe Ala Lys Ser Phe Ile Gly Ile Val Ser Ile Phe
195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Val Gly Phe Leu Leu Gly Asn
245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
260 265 270

Val Val Leu Gly Ser Lys Asn Lys Ala Cys Ser Val Val Phe Met Phe
275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Ala Pro Gly
325 330 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
420 425 430

Gly Cys Tyr Val Tyr Glu Leu Val Asn Arg Ile Thr Trp Glu Met Thr
435 440 445

Trp Phe Ser Asp His Cys His Gln Tyr Arg Ile Pro Cys Pro Tyr Gln
450 455 460

Ala Asn Pro Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Gly
530 535 540

Ala Pro Gly Pro His Arg Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545 550 555 560

Ser Thr Gly Ala Thr Thr Asn His Gly Thr Ser Ala Met Ala Ile Ala
565 570 575

Asp His Asp Tyr Leu Gly Gln Glu Thr Ser Thr Glu Val His Thr Ser
580 585 590

Pro Glu Ala Ser Val Lys Glu Gly Arg Ala Asp Arg Ala Asn Thr Pro
595 600 605

Ser Ala Lys Asp Arg Asp Cys Gly Glu Ser Ala Gly Pro Ser Ser Lys
610 615 620

Leu Ser Gly Asn Arg Asn Gly Arg Glu Ser Arg Ala Gly Gly Leu Lys
625 630 635 640

Glu Arg Ser Asn Gly Ser Glu Gly Ala Pro Ser Glu Gly Arg Val Ser
645 650 655

Pro Lys Ser Ser Val Pro Glu Thr Gly Leu Ile Asp Cys Ser Thr Ser
660 665 670

Gln Ala Ala Ser Ser Pro Glu Pro Thr Ser Leu Lys Gly Ser Thr Ser
675 680 685

Leu Pro Val His Ser Ala Ser Arg Ala Arg Lys Glu Gln Gly Ala Gly
690 695 700

Ser His Ser Asp Ala
705

<210> 36
<211> 2039
<212> DNA
<213> Homo sapiens

<400> 36
aggagacaac attagtggag tttgctttgt tggcctttat gacctggatg cttctcgcta
60
ctttgtactc ttgccactgt gcctttgtgt gtttgttggg ctctctcttc ttttagctgg
120
cattatttcc ttaaatcatg ttgcacaagt catacaacat gatggccgga accaagaaaa
180
actaaagaaa tttatgattc gaattggagt cttcagcggc ttgtatcttgc tgccattagt
240
gacacttctc ggatgttacg tctatgagca agtgaacagg attacctggg agataacttg
300
ggtctctgat cattgtcgtc agtaccatat cccatgtct tatcaggcaa aagcaaaagc
360
tcgaccagaa ttggctttat ttatgataaa atacctgatg acattaatttgc ttggcatctc
420
tgctgtcttc tgggttggaa gcaaaaagac atgcacagaa tgggctgggt tttttaaacg
480
aaatcgcaag agagatccaa tcagtgaaag tcgaagagta ctacaggaat catgtgagtt
540
tttcttaaag cacaattcta aagttaaaca caaaaagaag cactataaac caagttcaca
600
caagctgaag gtcatttcca aatccatggg aaccagcaca ggagctacag caaatcatgg
660
cacttctgca gtagcaatta ctagccatga ttaccttagga caagaaactt tgacagaaat
720
ccaaacctca ccagaaacat caatgagaga ggtgaaagcg gacggagcta gcaccccccag
780
gttaagagaa caggactgtg gtgaacctgc ctcgcccagca gcatccatct ccagactctc
840
tggggAACAG gtcgacggga agggccaggc aggcagtgtt cttgaaagtgc cgccggagtgc
900
aggaaggatt agtccaaaga gtgatattac tgacactggc ctggcacaga gcaacaattt
960
gcaggtcccc agttcttcag aaccaagcag cctcaaagggt tccacatctc tgcttggtca
1020

<210> 37
<211> 706
<212> PRT
<213> Homo sapiens

<400> 37

Met Glu Met Phe Thr Phe Leu Leu Thr Cys Ile Phe Leu Pro Leu Leu
1 5 10 15

Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65 70 75 80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
85 90 95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
115 120 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
130 135 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145 150 155 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
165 170 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
180 185 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe
195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp
245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
260 265 270

Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu
275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly
325 330 335

Phe Leu Thr Val Met Leu Ala Met Asn Lys Val Glu Gly Asp Asn
340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
420 425 430

Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr
435 440 445

Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln
450 455 460

Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr
530 535 540

Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545 550 555 560

Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr
565 570 575

Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser
580 585 590

Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro
595 600 605

Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser
610 615 620

Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly
625 630 635 640

Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser
645 650 655

Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro
660 665 670

Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val
675 680 685

His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Cys His Ser
690 695 700

Asp Thr
705

<210> 38
<211> 773
<212> DNA
<213> Murinae gen. sp.

<400> 38
ctgagggtgct agcaccagcc tgggtgtctc tggcgccct gaagcaagca tggatcaaga
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ggctgtggc aacgttgtgc tcctggccct tgtcaccctc atcagcgtgg tccagaatgc
120

gttcttgcc cacaagggtgg agcatgaaag caaggcgcat aatgggagaa gcttccagag
180

gaccggact cttgccttg agcgggtcta cactgccaac cagaactgcg tagatgcgta
240

ccccacttc cttgtggta cttggactgc aggactactt tgcagccaag tccctgcagc
300

cttcgcccga ctgatgtacc tgtttgcgat gcaaaaatac tttgtcggt atctggaga
360

gagaactcag agcacccctg gctacatctt cggcaagcgg atcatcctgt tcctgttct
420

catgtccttc gccgggatac tcaaccatta cctcatctc ttcttcggaa gcgactttga
480

gaactacatc agaacggtaa gcacgacgat ctccccgtg cttctcatcc cctgattgct
540

ggagacagag aaggacgctc accagatcaa tagagacgca tcataacgca acgcccggaa
600

ggcttctgct cctttcaag ctgttagatgc tgtcaatctt gctgccctcg gggctctgtg
660

gcattccgtta actttgcttt tccgggaaga aaaatgtctt gtgctaagct ccacccctcg
720

aatgcggcgg tggccagga tttatgtcta catccagcct atacttctcc tgg
773

<210> 39
<211> 852
<212> DNA
<213> Murinae gen. sp.

<400> 39
ggaaggctga ggtgcttagca ccagcctggc tgtctctggc gggcctgaag caagcatgga
60

tcaagaggct gtgggcaacg ttgtgctcct ggccttgc accctcatca gcgtggtcca
120

gaatgtgttt tttgcccact atgtggagca taaaagcaat ggcataatg ggagaagctt
180

ccagaggacc gggactcttg ctttgagcg ggtctacact gccaaccaga actgcgtaga
240

tgcgtacccc actttccttg tggtaactctg gactgcagga ctactttgca gccaagtccc
300

tgccgccttc gccggactga tgtacctgtt tgtgaggcaa aaatacttg tcggctatct
360

gggagagaga actcagagca cccctggcta catcttcggc aagcggatca tcctgttcct
420

gttcctcatg tccttcgccc ggatactcaa ccattacctc atcttcttct tcggaagcga
480

ctttgagaac tacatcagaa cggttaagcac gacgatctcc ccgctgcttc tcatccctg
540

attgctggag acagagaagg acgctcacca gatcaataga gacgcacat aacgcaacgc
600

cgcgaaggct tctgctcctc ttcaagctgt agatgctgtc aatcttgctg ccctcggggc
660

tctgtggcat ccgttaactt tgctttccg ggaagaaaaa tgtcttgta tagctccacc
720

cctcgaatgc ggcggtggcc caggattat tgtctacatc cagcctatac ttctcctggc
780

ttatcctgct ttctgaagat gtcttgtaat cagacacgtg tttcctaaa ataaaggta
840

tagacaaaaat tt
852

<210> 40
<211> 161
<212> PRT
<213> Murinae gen. sp.

<400> 40

Met Asp Gln Glu Ala Val Gly Asn Val Val Val Leu Leu Ala Leu Val Thr
1 5 10 15

Leu Ile Ser Val Val Gln Asn Val Phe Phe Ala His Tyr Val Glu His
20 25 30

Glu Ser Asn Ala His Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
50 55 60

Pro Thr Phe Leu Val Val Leu Trp Thr Ala Gly Leu Leu Cys Ser Gln
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Phe Ala
115 120 125

Gly Ile Leu Asn His Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
130 135 140

Asn Tyr Ile Arg Thr Val Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145 150 155 160

Pro

<210> 41

<211> 873

<212> DNA

<213> Homo sapiens

<400> 41

acttcccctt cctgtacagg gcaggttgtg cagctggagg cagagcagtc ctctctgggg
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agcctgaagc aaacatggat caagaaactg taggcaatgt tgtcctgttg gccatcgtca
120

ccctcatcag cgtggtccag aatggattct ttgccataa agtggagcac gaaagcagga
180

cccagaatgg gaggagcttc cagaggaccg gaacacttgc cttttagcgg gtctacactg
240

ccaaccagaa ctgtgttagat gcgtaccca ctttctcgc tgtgctctgg tctgcggggc
300

tactttgcag ccaagttcct gctgcgttg ctggactgat gtacttgtt gtgaggcaaa
360

agtactttgt cggttaccta ggagagagaa cgcagagcac ccctggctac atattggaa
420

aacgcatcat actcttcctg ttcctcatgt ccgttgctgg catattcaac tattaccta
480

tcttctttt cggaagtgac tttgaaaact acataaagac gatctcoacc accatctccc
540

ctctacttct cattccctaa ctctctgctg aatatgggt tggtgttctc atctaataaa
600

tacctacaag tcatcataat tcagctttg agagcattct gctttttt agatggctgt
660

aatctattg gccatctggg cttcacagct tgagttaacc ttgctttcc gggAACAAAA
720

tgatgtcatg tcagctccgc cccttgaaca tgaccgtggc cccaaatttg ctattccat
780

gcattttgtt tgtttcttca cttatcctgt tctctgaaga tgttttgtga ccaggttgt
840

gttttcttaa aataaaatgc agagacatgt ttt
873

<210> 42
<211> 161
<212> PRT
<213> Homo sapiens

<400> 42

Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr
1 5 10 15

Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His
20 25 30

Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
50 55 60

Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala
115 120 125

Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
130 135 140

Asn Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145 150 155 160

Pro

<210> 43
<211> 803
<212> DNA
<213> Murinae gen. sp.

<400> 43
ttcagcttta tgggttggct tccttgactg cattttctgt cagtttaacta aactccagac
60

tcatggattt tctcgaccag aaaatcagac tattttcctg aataatctac tagaaacttt
120

tacggaacac atttcatgtt tcctttgaag agttaagaga agaaagtatt tgtaagaaca
180

ggaaaagaaa caaatacttt gcaaataaac tggctgctgc tgtgaccaca tctgaatagc
240

aaaggcgatc gatcaagcgc tgccggacaaa aggccctcctg taagctgcac tgcctgacaa
300

tggtaagctc caatggctcc cagtgccctt atgacgactc cttaaagtac actctgtacg
360

ggtgcattgtt cagcatggtc ttctgtgcttg ggctgatatac caactgtgtt gcgatataca
420

ttttcatctg tgccctcaaa gtgagaaatg aaactacaac gtacatgatt aacctggcaa
480

tgtcagattt acttttcgtc tttactttgc catttcggat tttttacttt gcaacacgga
540

attggccatt tggagatcta ctctgtttaa tttcagtaat gctgtttac accaatatgt
600

atgggaagca ttctgttctt aacctgtatc agttagatc gatttctggc aattgtctac
660

ccatttaagt caaagacttt aagaaacgaa acgaaaatgc aaagaatgt ttgcattgcc
720

tgtgtggttc acagtgtatgg gaggaaagtgc gctgcagttt tctttcagtc gaccactct
780

caggggaaca atactcagaa gct
803

<210> 44
<211> 1849
<212> DNA
<213> Murinae gen. sp.

<400> 44
agagacagcc catctcacaa tacagctggc aacctccgaa aggccctctcc attcagcaag
60

cgcgaacatg cttaggaatt tatctggat cccttaaacg actgcctatc gccgtccgga
120

atcaatgtag aaatacaaag tttgagaata aaaagaagga agaagtaccc gaggacgacg
180

ggcggacgga cgcacggcga gtgttgtga ctgaagtaaa gctggttgg accctggcgg
240

ctgaagcaca agtttccacg cggactggtc tggtccgact tggAACAGTT tttccttaca
300

ctttcagctt tatgggttgg cttccttgac tgcattttct gtcagttaac taaactccag
360

actcatggat tttctcgacc agaaaatcag actatTTCC tgaataatct actagaaaact
420

tttacggaac acatttcatg tttccttga agagttttaa gaagaaagtA tttgttaagaa
480

cagggaaaaga aacaaatact ttgcaaataa actggctgct gctgtgacca catctgaata
540

gcaaaggcga tcgatcaagc gctgcggaca aaaggcctcc tgtaagctgc actgcctgac
600

aatggtaagc tccaaatggct cccagtgcCc ttatgacgac tccttaagt acactctgta
660

cgggtgcAtg ttcagcatgg tcttcgtgct tgggctgata tccaaCTgtg ttgcgatata
720

cattttcatc tgtgccctca aagtggaaa tggAAactaca acgtacatga ttaacctggc
780

aatgtcagat ttactttcg tctttacttt gccatttcgg atttttact ttgcaacacg
840

gaattggcca tttggagatc tactctgtaa gatttcagta atgctgttt acaccaata
900

gtatggaaagc attctgttct taacctgtat cagtgttagat cgatttctgg caattgtcta
960

cccatttaag tcaaagactt taagaacgaa acgaaatgca aagatcgTTT gcattgtgt
1020

gtggttcaca gtgatggag gaagtgcGCC tgcagtttc tttcagtcga cccactctca
1080

gggaaacaat acctcagaag cctgcttga gaactttcca gcccacat ggaaaactta
1140

tctctccagg attgtgattt tcattgaaat agtgggcttt tttatccctc tcattttgaa
1200

cgttaacttgt tctagtatgg tgctaagaac ttAAataaaa cctgttacat taagtagaag
1260

caaaatgaac aaaactaagg ttttaaaaat gattttgtc cacttggtca tcttctgttt
1320

ctgtttgtg ccctacaaca tcaacctcat tttgtactcg ctcatgagga cacagacctt
1380

tgttaactgc tctgtggtgg cggcagttag gaccatgtac ccgatcactc tctgcacgc
1440

tgtttccaac tgctgctttg accctattgt ttactacttc acctcagaca caattcagaa
1500

ctcaataaaa atgaaaaact ggtcggttag aagaagttag tccaggtct ctgaagttca
1560

gggcactgag aattttatcc aacacaacct acagacctta aaaaataaga tatttgataa
1620

tgaatctgca atataagctg cctgactaag ccactgggac tgctccgtgt tcaactgtga
1680

aaactgtgtt cttggaaact atctctccgg ctccaacaga aaatatttt aaaggaagtt
1740

tgtgtctgat gtgttaaaca ttaaaatata ttctattctt gtatgcacgc cattttactt
1800

tcttgaacca cttaacgtg tttttcctc attaaaaaaa aaaaactcc
1849

<210> 45
<211> 316
<212> PRT
<213> Murinae gen. sp.

<400> 45

Asp	Asp	Ser	Phe	Lys	Tyr	Thr	Leu	Tyr	Gly	Cys	Met	Phe	Ser	Met	Val
1															15

Phe	Val	Leu	Gly	Leu	Ile	Ser	Asn	Cys	Val	Ala	Ile	Tyr	Ile	Phe	Ile
															20
															25
															30

Cys	Ala	Leu	Lys	Val	Arg	Asn	Glu	Thr	Thr	Thr	Tyr	Met	Ile	Asn	Leu
															35
															40
															45

Ala	Met	Ser	Asp	Leu	Leu	Phe	Val	Phe	Thr	Leu	Pro	Phe	Arg	Ile	Phe
															50
															55
															60

Tyr	Phe	Ala	Thr	Arg	Asn	Trp	Pro	Phe	Gly	Asp	Leu	Leu	Cys	Lys	Ile
															65
															70
															75
															80

Ser	Val	Met	Leu	Phe	Tyr	Thr	Asn	Met	Tyr	Gly	Ser	Ile	Leu	Phe	Leu
															85
															90
															95

Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys
100 105 110

Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala Lys Ile Val Cys Ile Ala
115 120 125

Val Trp Phe Thr Val Met Gly Gly Ser Ala Pro Ala Val Phe Phe Gln
130 135 140

Ser Thr His Ser Gln Gly Asn Asn Thr Ser Glu Ala Cys Phe Glu Asn
145 150 155 160

Phe Pro Ala Ala Thr Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe
165 170 175

Ile Glu Ile Val Gly Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys
180 185 190

Ser Ser Met Val Leu Arg Thr Leu Asn Lys Pro Val Thr Leu Ser Arg
195 200 205

Ser Lys Met Asn Lys Thr Lys Val Leu Lys Met Ile Phe Val His Leu
210 215 220

Val Ile Phe Cys Phe Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu
225 230 235 240

Tyr Ser Leu Met Arg Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala
245 250 255

Ala Val Arg Thr Met Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn
260 265 270

Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln
275 280 285

Asn Ser Ile Lys Met Lys Asn Trp Ser Val Arg Arg Ser Asp Ser Arg
290 295 300

Phe Ser Glu Val Gln Gly Thr Glu Asn Phe Ile Gln
305 310 315

<210> 46

<211> 1035

<212> DNA

<213> Homo sapiens

<400> 46 .
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120
atttcatct gcgtcctcaa agtccgaaat gaaactacaa cttacatgtat taacttggca
180
atgtcagact tgcttttgc ttttacttta cccttcagga tttttactt cacaacacgg
240
aattggccat ttggagattt actttgtaag atttctgtga tgctgttttaccaacatg
300
tacggaagca ttctgttctt aacctgtatt agttagatc gatttctggc aattgtctac
360
ccatttaagt caaagactct aagaaccaaa agaaatgcaa agattgttttgc aactggcgtg
420
tggtaactg tgatcgagg aagtgcaccc gccgttttg ttcaagtctac ccactctcag
480
ggtaacaatg cctcagaagc ctgctttgaa aattttccag aagccacatg gaaaacatat
540
ctctcaagga ttgttaatttt catgaaataa gtgggatttt ttattcctct aattttaaat
600
gtaacttgc ttgtatggt gctaaaaact ttaaccaaac ctgttacatt aagtagaagc
660
aaaataaaaca aaactaagg tttaaaaatg attttgtac atttgatcat attctgtttc
720
tgttttgttc cttacaatat caatcttatt ttatattctc ttgtgagaac acaaacattt
780
gttaattgct cagtagtggc agcagtaagg acaatgtacc caatcactct ctgtattgct
840
gtttccaaact gttgttttga ccctatagtt tactacttta catcgacac aattcagaat
900
tcaataaaaa tgaaaaactg gtctgtcagg agaagtgact tcagattctc tgaagttcat
960
ggtgcagaga attttattca gcataaccta cagacctaa aaagtaagat atttgacaat
1020
gaatctgctg cctga
1035

<210> 47
<211> 344
<212> PRT
<213> Homo sapiens

<400> 47

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys
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Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu
20 25 30

Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val
35 40 45

Arg Asn Glu Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu
50 55 60

Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg
65 70 75 80

Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe
85 90 95

Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val
100 105 110

Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg
115 120 125

Thr Lys Arg Asn Ala Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val
130 135 140

Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln
145 150 155 160

Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr
165 170 175

Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly
180 185 190

Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu
195 200 205

Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys
210 215 220

Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe
225 230 235 240

Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg
245 250 255

Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met
260 265 270

Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro
275 280 285

Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met
290 295 300

Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His
305 310 315 320

Gly Ala Glu Asn Phe Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys
325 330 335

Ile Phe Asp Asn Glu Ser Ala Ala
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<210> 48

<211> 814

<212> DNA

<213> Murinae gen. sp.

<400> 48

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120

tccccaaaca gccagtcacc acctctgtcc cctcttcaact gttggtcgtc agactgcctg
180

agtggacagc aggctggtcg cgttgtatTT tcacttcctt cctctgactg gcttgctctt
240

gtctctcagt ctttcatccc aggcagctgc ctgaggtagg tgaggaggat ggtgagccag
300

gcaggtctac aataaaggca gctctgtccg gtccttctg gtcgtgagt gtcaccggcc
360

tggaagactg aggaaatggc tccctctct cctcccccgtc tttccccagt tcctcccta
420

tgttgccca tgtgcccagg gagttggaag catcagggag accctcttag tgtgggaaag
480

gaagtcagag accattgaca cagtgaagag gcaggatcat gtgttggaaag cctgttagca
540

ggaccaaggt gactcttggg agagactctt gtggacacag gccgtggtgg cttgtcagac
600

cttaaagggt ccaggcccac ccctgccagg atccctggtc tgctttctcc aggacacact
660

gggacactgc tgagtaatga gcagcttatt acacacaatg ggaagagggg cagagagggc
720

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780

gagcctggct acctgtcttt accccttcaa ggac
814

<210> 49

<211> 1164

<212> DNA

<213> Murinae gen. sp.

<400> 49

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120

cagccagcc tcttggggtt caggagggtc ctgcagaaac tccagacgga cggactcaag
180

gagtgcatta tcttctgcgt gcgggaggag cctgtgggtgt tcttgcgccgc tgaggaggac
240

tttgtgtctt acacacctcg agacaaggag agcattcatg agaacacctcg ggaccctagt
300

ccaggggtca aggctgagaa tctggagctg gccatccaga aagagatcca tgactttgcc
360

caattgagag ataatgtgtt ccacgtatac cacaacacag aggacctgcg cggggagccg
420

cacacgtgg ccatccgagg tgaggatggc gtgtgcgtga ccgaggaggt gtttaagcgg
480

ccgctcttcc tgcagccac ctacagatac caccgcctcc cttgcaga gcaagggcc
540

cccctggaag cccagttga tgccttgcgtc agcgtttttc gggagacccc cagccttctg
600

ccactcagag ataaccacgg gcctctgcct gccctcctgt tcagctgcca gtcaggtgt
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ggcagaacca acctaggcat ggtcctggaa accctcgta tggccacca cagtaggacc
720

acctcccagc tagaggcagc ctccccgttg gccaaacccc tgcccatgga gcagttcag
780

gtgatccagg gcttcatctg taaggtgcca cagggaaaga aaatggtgga ggaggtggat
840

cgagcgatca gtgcctgtgc agagttgcat gacctgaagg aggaggtcct aaaaaaaccag
900

aggaggctgg aaagcttcag gccagagagc cggggacagg aatgtggtag tcagcaagct
960

gtccagcaga gggcgctgtg gagcctggag ctgtacttct atctgctcct atttaactac
1020

tatctgcatg agcagtaccc cctggcctt gccctcagtt tcagtcgatg gctgtgtacc
1080

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<210> 50

<211> 388

<212> PRT

<213> Murinae gen. sp.

<400> 50

Gly Arg Tyr Phe Leu Val Arg Asp Ile Thr Glu Lys Met Asp Ile Leu
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Gly Thr Leu Lys Ser Cys Gly Ala Pro Asn Phe Arg Gln Val Arg Gly
20 25 30

Gly Leu Pro Val Phe Gly Met Gly Gln Pro Ser Leu Leu Gly Phe Arg
35 40 45

Arg Val Leu Gln Lys Leu Gln Thr Asp Gly Leu Lys Glu Cys Ile Ile
50 55 60

Phe Cys Val Arg Glu Glu Pro Val Val Phe Leu Arg Ala Glu Glu Asp
65 70 75 80

Phe Val Ser Tyr Thr Pro Arg Asp Lys Glu Ser Leu His Glu Asn Leu
85 90 95

Arg Asp Pro Ser Pro Gly Val Lys Ala Glu Asn Leu Glu Leu Ala Ile
100 105 110

Gln Lys Glu Ile His Asp Phe Ala Gln Leu Arg Asp Asn Val Tyr His

115

120

125

Val Tyr His Asn Thr Glu Asp Leu Arg Gly Glu Pro His Thr Val Ala
130 135 140

Ile Arg Gly Glu Asp Gly Val Cys Val Thr Glu Glu Val Phe Lys Arg
145 150 155 160

Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg Leu Pro Leu Pro
165 170 175

Glu Gln Gly Ala Pro Leu Glu Ala Gln Phe Asp Ala Phe Val Ser Val
180 185 190

Leu Arg Glu Thr Pro Ser Leu Leu Pro Leu Arg Asp Asn His Gly Pro
195 200 205

Leu Pro Ala Leu Leu Phe Ser Cys Gln Ser Gly Val Gly Arg Thr Asn
210 215 220

Leu Gly Met Val Leu Gly Thr Leu Val Met Phe His His Ser Arg Thr
225 230 235 240

Thr Ser Gln Leu Glu Ala Ala Ser Pro Leu Ala Lys Pro Leu Pro Met
245 250 255

Glu Gln Phe Gln Val Ile Gln Gly Phe Ile Cys Lys Val Pro Gln Gly
260 265 270

Lys Lys Met Val Glu Glu Val Asp Arg Ala Ile Ser Ala Cys Ala Glu
275 280 285

Leu His Asp Leu Lys Glu Glu Val Leu Lys Asn Gln Arg Arg Leu Glu
290 295 300

Ser Phe Arg Pro Glu Ser Arg Gly Gln Glu Cys Gly Ser Gln Gln Ala
305 310 315 320

Val Gln Gln Arg Ala Leu Trp Ser Leu Glu Leu Tyr Phe Tyr Leu Leu
325 330 335

Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu Ala Phe Ala Leu
340 345 350

Ser Phe Ser Arg Trp Leu Cys Thr His Pro Glu Leu Tyr Arg Leu Leu
355 360 365

Val Glu Leu Asn Ser Val Gly Pro Leu Val Pro Gly Asp Leu Ile Ala
370 375 380

Lys Gly Ser Leu
385

<210> 51
<211> 4303
<212> DNA
<213> Homo sapiens

<400> 51
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1080

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1980

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2100

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2280

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4260

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4303

<210> 52
<211> 861
<212> PRT
<213> Homo sapiens

<400> 52

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Asp Ser Arg His Ser Val Ser Ile His Ser Phe Gln Ser Thr Ser Leu
35 40 45

His Asn Ser Lys Ala Lys Ser Ile Ile Pro Asn Lys Val Ala Pro Val
50 55 60

Val Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu
65 70 75 80

Leu Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu
85 90 95

His Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu
100 105 110

Lys Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe
115 120 125

Arg Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser
130 135 140

Leu Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His
145 150 155 160

Arg Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu
165 170 175

Arg Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn
180 185 190

Leu His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser
195 200 205

Leu Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser
210 215 220

Glu Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu
225 230 235 240

Pro His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu
245 250 255

Glu Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His
260 265 270

Arg Leu Pro Leu Pro Glu Gln Gly Ser Pro Leu Glu Ala Gln Leu Asp
275 280 285

Ala Phe Val Ser Val Leu Arg Glu Thr Pro Ser Leu Leu Gln Leu Arg
290 295 300

Asp Ala His Gly Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly
305 310 315 320

Val Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu
325 330 335

His Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala
340 345 350

Lys Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg
355 360 365

Met Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile
370 375 380

Thr Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn
385 390 395 400

Gln Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser
405 410 415

Gly Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg
420 425 430

Tyr Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro
435 440 445

Leu Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu
450 455 460

Leu Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro
465 470 475 480

Arg Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser
485 490 495

Pro Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg
500 505 510

Arg Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys
515 520 525

Ala Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu
530 535 540

Arg Lys Val Val Trp Val Ser Leu Arg Glu Glu Ala Val Leu Glu Cys
545 550 555 560

Asp Gly His Thr Tyr Ser Leu Arg Trp Pro Gly Pro Pro Val Ala Pro
565 570 575

Asp Gln Leu Glu Thr Leu Glu Ala Gln Leu Lys Ala His Leu Ser Glu
580 585 590

Pro Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys
595 600 605

Leu Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly
610 615 620

Leu Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu
625 630 635 640

Glu Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys
645 650 655

Asp Pro Gly Thr Gly Phe Val Phe Ser Cys Leu Ser Gly Gln Gly Arg
660 665 670

Thr Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln
675 680 685

Gly Phe Pro Glu Val Gly Glu Glu Leu Val Ser Val Pro Asp Ala
690 695 700

Lys Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu
705 710 715 720

Leu Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp
725 730 735

Thr Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile

740 745 750

Ile Ile Cys Thr Tyr Arg Gln Ala Lys Ala Ala Lys Glu Ala Gln Glu
755 760 765

Met Arg Arg Leu Gln Leu Arg Ser Leu Gln Tyr Leu Glu Arg Tyr Val
770 775 780

Cys Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser
785 790 795 800

Trp Gln Arg Pro Phe Ser Thr Trp Met Gln Glu Val Ala Ser Lys Ala
805 810 815

Gly Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser
820 825 830

Gly Glu Asp Gln Pro Phe Ser Arg Leu Arg Tyr Arg Trp Gln Glu Gln
835 840 845

Ser Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu
850 855 860